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FIGURE 1

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IGURE 2

\vdash	MOORGLAIVALAVCAALHASEAILPIASS 4185824 MNLWLLACLVAGFLGAWAPAVHTQGVFED GI 2388627
98	CCTEVSHHISRRLLERVNMCRIQRADGDC 4185824 CCLAYHYPIGWAVLRRAWTYRIQEVSGSC GI 2388627
29	DLAAVILHUKRRRICVSPHNHTVKOWM 4185824 NLPAAIFYLPKRHRKVCGNPKSREVQRAM GI 2388627
88	KVQAAKKNGKGNVCHRKK HHGKR 4185824 KLLDARNKVFAKLHHNMQTFQAGPHAVKK GI 2388627
109	DSNRAHQGKHETYGH4185824 LSGNSKLSSKFSNPISSKRNVSLLIS GI 2388627
124 146	- K T P Y A N S G L GI 2388627

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2484440 g853834	2484440 g853834	2484440 g853834	2484440 g853834	2484440 g853834	2484440 g853834	2484440 g853834	2484440 g853834
1 M ERGAHGGA 1 MLNQRIHPGMLVLLMFLYHFMEDHTAQAGN	10GGCLCLLPEG31 CWLRQARNGRCQVLYKTDLSKEECCKSGRL	20FRILGVKGGS	30	30 LSEMSP 121 CSNITWKGPVCGLDGKTYRNECALLKARCK	44 EASP GTRPAESCEHVVCPRPQSCVV 151 EQPELEVQYQGKCKKTCRDVLCPGSSTCVV	69 DOTGSAHCVVCRAAPCPVPSSPGQELCGNN 181 DOTNNAYCVTCNRI-CPEPTSPEQYLCGND	99 NVTYISSCHMROATCFLGRSIG 210 GITYASACHLRKATCLLGRSIGLAYEGKCI
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FIGURE 3A

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2484440 DIQCSAGKKCLWDFKVGRGRCALC g853834		VRHAGSCAGTPEEPPGGESAE 2484440 LLEVKHSGSCNSINEDPEEEEDE 9853834	<u>V</u> P I S S I L E W g853834
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FIGURE 4